

SEARCH REQUEST FORM

Requester's Full Name: Jeffrey E. Russel Examiner #: 62785 Date: 4-26-2005
 Art Unit: 1654 Phone Number: 2-0969 Serial Number: 09/992,124
 Location (Bldg/Room#): REM 3D19 (Mailbox #): 3C18 Results Format Preferred (circle): PAPER DISK

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: Peptides Promoting Cell Adherence, Growth And Secretion

Inventors (please provide full names): R. Campbell, M. Heideran, C. Spargo, J. Wilkins, P. Hagland

Earliest Priority Date: 11-19-2001

Search Topic:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please search HK NQT (SEQ ID No: 34) in STN, in the U.S. patent application sequence database (pending, published, & issued) and in PIR/Unigra/Geneseq.

Thank you.

JER

STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher: _____	_____ NA Sequence (#)	_____ STN _____ Dialog
Searcher Phone #: _____	_____ AA Sequence (#)	_____ Questel/Orbit _____ Lexis/Nexis
Searcher Location: _____	_____ Structure (#)	_____ Westlaw _____ WWW/Internet
Date Searcher Picked Up: _____	_____ Bibliographic	_____ In-house sequence systems

=> fil reg; d que l3; d que l4; fil capl; d que l7
FILE 'REGISTRY' ENTERED AT 16:29:49 ON 27 APR 2005
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STRUCTURE FILE UPDATES: 26 APR 2005 HIGHEST RN 849322-79-8
DICTIONARY FILE UPDATES: 26 APR 2005 HIGHEST RN 849322-79-8

New CAS Information Use Policies, enter HELP USAGETERMS for details.

TSCA INFORMATION NOW CURRENT THROUGH JANUARY 18, 2005

Please note that search-term pricing does apply when
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*
* The CA roles and document type information have been removed from *
* the IDE default display format and the ED field has been added, *
* effective March 20, 2005. A new display format, IDERL, is now *
* available and contains the CA role and document type information. *
*

Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. For more
information enter HELP PROP at an arrow prompt in the file or refer
to the file summary sheet on the web at:
<http://www.cas.org/ONLINE/DBSS/registryss.html>

L3 433 SEA FILE=REGISTRY ABB=ON HKNQT/SQSP

L3 433 SEA FILE=REGISTRY ABB=ON HKNQT/SQSP
L4 0 SEA FILE=REGISTRY ABB=ON L3 AND SQL<11

FILE 'CAPLUS' ENTERED AT 16:29:49 ON 27 APR 2005
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FILE COVERS 1907 - 27 Apr 2005 VOL 142 ISS 18
FILE LAST UPDATED: 26 Apr 2005 (20050426/ED)

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This file contains CAS Registry Numbers for easy and accurate
substance identification.

'OBI' IS DEFAULT SEARCH FIELD FOR 'CAPLUS' FILE

L3 433 SEA FILE=REGISTRY ABB=ON HKNQT/SQSP
L5 173 SEA FILE=CAPLUS ABB=ON L3
L6 168797 SEA FILE=CAPLUS ABB=ON CELL?/OBI(L) (ADHE?/OBI OR GROW?/OBI OR
SECRET?/OBI)
L7 52 SEA FILE=CAPLUS ABB=ON L5 AND L6

=> d ibib ed abs hitseq l7 1-52; fil hom

L7 ANSWER 1 OF 52 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2005:260218 CAPLUS Full-text
DOCUMENT NUMBER: 142:334913
TITLE: Multi-tumor antigen-expressing vectors for preventing
and/or treating melanoma
INVENTOR(S): Berinstein, Neil; Tartaglia, Jim; Parrington, Mark;
Panicali, Dennis; Gritz, Linda
PATENT ASSIGNEE(S): Aventis Pasteur Limited, Can.; Therion Biologics, Inc.
SOURCE: PCT Int. Appl., 88 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2005026370	A2	20050324	WO 2004-US28751	20040903
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW			
RW:	BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			

PRIORITY APPLN. INFO.: US 2003-500572P P 20030905
US 2003-504007P P 20030918

ED Entered STN: 25 Mar 2005

AB The present invention provides multi-antigen vectors for administration to a patient to prevent and/or treat cancer. In particular, the invention relates to epitope peptides and nucleic acid sequences encoding such peptides for use in diagnosing, treating, or preventing melanoma. Provided are vectors for preventing and/or treating melanoma co-expressing immunogenic targets selected from NY-ESO-1, TRP-2, gp100, gp100M, a MART antigen, MART-1, a MAGE antigen, MAGE-1, and MAGE-3. The multi-antigen vector may also encode an immune

stimulator such as a co-stimulatory mol. and/or be administered with an adjuvant.

IT 848511-63-7P

RL: BPN (Biosynthetic preparation); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(amino acid sequence; multi-tumor antigen-expressing vectors for preventing and/or treating melanoma)

RN 848511-63-7 CAPLUS

CN Cell adhesion molecule ICAM-1 (intercellular adhesion mol. 1) (human)
(9CI) (CA INDEX NAME)

SEQ 1 MAPSSPRPAL PALLVLLGAL FPGPGNAQTS VSPSKVILPR GGSVLVTCST
51 SCDQPKLLGI ETPLPKKELL LPGNNRKVYE LSNVQEDSQP MCYSNCPDGQ
101 STAKTFLTVY WTPERVELAP LPSWQPVGKN LTLRCQVEGG APRANLTVVL
151 LRGEKELKRE PAVGEPAEVT TTVLVRRDHH GANFSCRTTEL DLRPQGLELF
201 ENTSAPYQLQ TFLVPATPPQ LVSPRVLEVD TQGTVVCSLD GLFPVSEAQV
251 HLAIGDQRLN PTVTYGNDSF SAKASVSVTA EDEGTQRLTC AVILGNQSQE
301 TLQTVTIYSF PPNVILTKP EVSEGTEVTV KCEAHPRAKV TLNGVPAQPL
351 GPRAQLLLKA TPEDNGRSFS CSATLEVAGQ LIHKNQTREL RVLYGPRLDE
401 RDCPGNWTWP ENSQQTPMCQ AWCNPLPELK CLKDGTFFLP IGESVTVTRD
451 LEGTYLCRAR STQGEVTREV TVNVLSPRYE IVIITVVAHA VIMGTAGLST
501 YLYNRQRKIK KYRLQQAQKG TPMKPNTQAT PP

L7 ANSWER 2 OF 52 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2005:232398 CAPLUS Full-text

DOCUMENT NUMBER: 142:310962

TITLE: Methods for identifying genes associated with enhanced resistance to HIV1 or HCV infection in primates and targets for therapy

INVENTOR(S): Messier, Walter; Sikela, James

PATENT ASSIGNEE(S): Evolutionary Genomics, LLC, USA

SOURCE: U.S., 98 pp., Cont.-in-part of U.S. Ser. No. 942,252.
CODEN: USXXAM

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 10

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 6866996	B1	20050315	US 2002-98600	20020314
US 6228586	B1	20010508	US 1999-240915	19990129
US 6280953	B1	20010828	US 2000-591435	20000609
US 2005037400	A1	20050217	US 2004-883576	20040630
PRIORITY APPLN. INFO.:			US 1998-73263P	P 19980130
			US 1998-98987P	P 19980902
			US 1999-240915	A2 19990129
			US 2000-591435	A2 20000609
			US 2001-942252	A2 20010828
			US 2002-98600	A2 20020314
			US 2003-484030P	P 20030630
			US 2004-545604P	P 20040217

ED Entered STN: 17 Mar 2005

AB The present invention provides methods for identifying evolutionarily significant polynucleotide and polypeptide sequences in human and/or non-human primates which may be associated with a physiol. condition, such as enhanced

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=> d his full

(FILE 'HOME' ENTERED AT 16:18:57 ON 27 APR 2005)

FILE 'LREGISTRY' ENTERED AT 16:19:12 ON 27 APR 2005

L1 0 SEA ABB=ON HKNQT/SQSP
L2 6 SEA ABB=ON HKNQT/SQSFP
D SQIDE 1-6

FILE 'REGISTRY' ENTERED AT 16:19:50 ON 27 APR 2005

L3 433 SEA ABB=ON HKNQT/SQSP
SAVE TEMP L3 RUS124SEQ1/A
L4 0 SEA ABB=ON L3 AND SQL<11

FILE 'CAPLUS' ENTERED AT 16:20:37 ON 27 APR 2005

L5 173 SEA ABB=ON L3
L6 168797 SEA ABB=ON CELL?/OBI(L) (ADHE?/OBI OR GROW?/OBI OR SECRET?/OBI)
L7 52 SEA ABB=ON L5 AND L6

FILE 'REGISTRY' ENTERED AT 16:22:38 ON 27 APR 2005

FILE 'REGISTRY' ENTERED AT 16:23:00 ON 27 APR 2005
D QUE

FILE 'REGISTRY' ENTERED AT 16:23:22 ON 27 APR 2005
D QUE L3
D QUE L4

FILE 'CAPLUS' ENTERED AT 16:23:22 ON 27 APR 2005
D QUE L7
D IBIB ED ABS HITSEQ L7
D IBIB ED ABS HITRN 2-52
SEL HIT RN L7 1-52

FILE 'REGISTRY' ENTERED AT 16:29:49 ON 27 APR 2005
D QUE L3
D QUE L4

FILE 'CAPLUS' ENTERED AT 16:29:49 ON 27 APR 2005
D QUE L7
D IBIB ED ABS HITSEQ L7 1-52

FILE 'HOME' ENTERED AT 16:30:39 ON 27 APR 2005

FILE HOME

FILE LREGISTRY
LREGISTRY IS A STATIC LEARNING FILE

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FILE REGISTRY
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STRUCTURE FILE UPDATES: 26 APR 2005 HIGHEST RN 849322-79-8

DICTIONARY FILE UPDATES: 26 APR 2005 HIGHEST RN 849322-79-8

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*****
*
* The CA roles and document type information have been removed from *
* the IDE default display format and the ED field has been added, *
* effective March 20, 2005. A new display format, IDERL, is now *
* available and contains the CA role and document type information. *
*
*****
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Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. For more
information enter HELP PROP at an arrow prompt in the file or refer
to the file summary sheet on the web at:

<http://www.cas.org/ONLINE/DBSS/registryss.html>

FILE CAPLUS

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FILE LAST UPDATED: 26 Apr 2005 (20050426/ED)

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OM protein - protein search, using sw model

Run on: April 27, 2005, 18:56:18 ; Search time 38 Seconds
(without alignments)
12.660 Million cell updates/sec

Title: US-09-992-124C-34
Perfect score: 29
Sequence: 1 HKNQT 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	29	100.0	278	2	A84545	hypothetical prote
2	29	100.0	320	2	T30894	lipase homolog T0
3	29	100.0	532	1	A29849	intercellular adhe
4	29	100.0	677	2	G69895	formate dehydrogen
5	29	100.0	989	2	T15397	hypothetical prote
6	29	100.0	1020	2	G88208	protein K02A2.3 [i
7	29	100.0	1075	1	OYRTHX	heat-stable entero
8	29	100.0	1516	2	T41235	probable myosin he
9	29	100.0	2201	2	A54774	ATP binding casset
10	26	89.7	167	2	AC0481	probable gluconoki
11	26	89.7	184	2	G83591	hypothetical prote
12	26	89.7	279	2	S55105	hypothetical prote
13	26	89.7	326	2	C86872	UDPglucose 4-epime

14	26	89.7	351	2	T19372	hypothetical prote
15	26	89.7	393	2	S48381	RRD1 protein - yea
16	26	89.7	411	2	D88504	protein B0361.7 [i
17	26	89.7	416	2	G86488	protein T32E20.31
18	26	89.7	481	2	JC7961	proton-coupled ami
19	26	89.7	519	2	T22091	hypothetical prote
20	26	89.7	530	2	F84905	probable cytochrom
21	26	89.7	717	1	VGBE11	glycoprotein H pre
22	26	89.7	779	2	C96805	hypothetical prote
23	26	89.7	783	2	T18421	hypothetical prote
24	26	89.7	873	2	S46584	probable membrane
25	26	89.7	890	2	T22186	hypothetical prote
26	26	89.7	1022	2	E84792	probable kinesin h
27	26	89.7	1029	2	T00712	protein kinase hom
28	26	89.7	1139	2	A49370	ElA-associated cyc
29	26	89.7	1291	2	T21694	hypothetical prote
30	26	89.7	1435	2	S59384	hypothetical prote
31	26	89.7	1577	2	A35140	hemolysin A precur
32	26	89.7	2588	2	T14342	NSD1 protein - mou
33	25	86.2	20	2	PN0115	insulin-like growt
34	25	86.2	63	2	S70821	H+-transporting tw
35	25	86.2	107	2	G85676	unknown protein en
36	25	86.2	107	2	C90817	hypothetical prote
37	25	86.2	121	2	H89903	conserved hypothet
38	25	86.2	193	2	S63689	dehydrin-like prot
39	25	86.2	227	2	C81346	tonB transport pro
40	25	86.2	233	2	T39948	hypothetical prote
41	25	86.2	240	2	S59085	ribosomal protein
42	25	86.2	248	2	T26584	hypothetical prote
43	25	86.2	258	2	B49597	nonstructural prot
44	25	86.2	262	2	T22489	hypothetical prote
45	25	86.2	264	2	F89833	teichoic acid tran

ALIGNMENTS

RESULT 1

A84545

hypothetical protein At2g16850 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001

C;Accession: A84545

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Mason, T.M.; Bowman, C.L.; Barnstead, M.E.; Feldblyum, T.V.; Buell, C.R.; Ketchum, K.A.; Lee, J.J.; Ronning, C.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.J.; Gill, J.E.; Adams, M.D.; Carrera, A.J.; Creasy, T.H.; Goodman, H.M.; Somerville, C.R.; Copenhaver, G.P.; Preuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.C.

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: A84545

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-278 <STO>
A;Cross-references: GB:AE002093; NID:g3757514; PIDN:AAC64216.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2gl6850
A;Map position: 2
C;Superfamily: lens fiber membrane major intrinsic protein

Query Match 100.0%; Score 29; DB 2; Length 278;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKNQT 5
|||||
Db 59 HKNQT 63

Search completed: April 27, 2005, 19:05:48
Job time : 42 secs

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OM protein - protein search, using sw model

Run on: April 28, 2005, 12:07:02 ; Search time 176 Seconds
(without alignments)
14.548 Million cell updates/sec

Title: US-09-992-124C-34
Perfect score: 29
Sequence: 1 HKNQT 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 50

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%	Query				
No.	Score	Match	Length	DB	ID	Description	
1	29	100.0	130	2	Q972R5	Q972r5	sulfolobus
2	29	100.0	169	2	Q6YQ99	Q6yq99	onion yello
3	29	100.0	169	2	Q8A3B7	Q8a3b7	bacteroides
4	29	100.0	196	2	Q9GNM6	Q9gnm6	ostertagia
5	29	100.0	196	2	Q9N9C5	Q9n9c5	ostertagia
6	29	100.0	218	2	Q8A0X0	Q8a0x0	bacteroides
7	29	100.0	248	2	Q9BS20	Q9bs20	homo sapien
8	29	100.0	276	2	Q15463	Q15463	homo sapien
9	29	100.0	278	1	PI28_ARATH	Q9zvx8	arabidopsis
10	29	100.0	289	2	Q6QF96	Q6qf96	triticum ae
11	29	100.0	289	2	Q75RZ4	Q75rz4	triticum ae
12	29	100.0	297	2	Q805L2	Q805l2	saimiriine
13	29	100.0	297	2	Q80BH5	Q80bh5	saimiriine
14	29	100.0	297	2	Q80BM8	Q80bm8	saimiriine
15	29	100.0	297	2	Q80BR3	Q80br3	saimiriine
16	29	100.0	343	2	Q9C086	Q9c086	homo sapien
17	29	100.0	345	2	Q99PT3	Q99pt3	mus musculu
18	29	100.0	356	2	Q96B14	Q96b14	homo sapien
19	29	100.0	356	2	Q80ZV5	Q80zv5	mus musculu
20	29	100.0	366	2	Q6E5N8	Q6e5n8	ictalurus p
21	29	100.0	375	2	Q9CY38	Q9cy38	mus musculu
22	29	100.0	380	2	Q74IH0	Q74ih0	lactobacill
23	29	100.0	432	1	ORC4_XENLA	O93479	xenopus lae
24	29	100.0	432	2	Q6GL43	Q6gl43	xenopus tro
25	29	100.0	432	2	Q6NWF3	Q6nwf3	brachydanio
26	29	100.0	436	1	ORC4_HUMAN	O43929	homo sapien
27	29	100.0	449	2	Q7S4R6	Q7s4r6	neurospora
28	29	100.0	449	2	Q93EJ5	Q93ej5	bacillus li
29	29	100.0	449	2	Q65DH7	Q65dh7	bacillus li
30	29	100.0	479	2	Q6ARN7	Q6arn7	desulfotale
31	29	100.0	505	1	ICA1_PANTR	Q28806	pan troglod
32	29	100.0	532	1	ICA1_HUMAN	P05362	homo sapien
33	29	100.0	532	2	Q96B50	Q96b50	homo sapien
34	29	100.0	629	1	YX14_CAEEL	Q11125	caenorhabdi
35	29	100.0	677	2	O34323	O34323	bacillus su
36	29	100.0	679	2	Q65IQ5	Q65iq5	bacillus li
37	29	100.0	684	2	Q73KC2	Q73kc2	treponema d
38	29	100.0	772	2	Q9SY24	Q9sy24	arabidopsis
39	29	100.0	819	2	Q8W4M0	Q8w4m0	arabidopsis
40	29	100.0	1020	1	YRD3_CAEEL	Q09573	caenorhabdi
41	29	100.0	1072	1	HSER_RAT	P23897	rattus norv
42	29	100.0	1158	2	Q7Q253	Q7q253	anopheles g
43	29	100.0	1516	1	MY52_SCHPO	O94477	schizosacch
44	29	100.0	1678	2	Q8UW88	Q8uw88	oryzias lat
45	29	100.0	1815	2	Q7VI74	Q7vi74	helicobacte
46	29	100.0	2201	2	Q80ZB2	Q80zb2	rattus norv
47	29	100.0	2260	2	Q8UVV4	Q8uvv4	gallus gall
48	29	100.0	2261	1	ABC1_HUMAN	O95477	homo sapien
49	29	100.0	2261	1	ABC1_MOUSE	P41233	mus musculu
50	29	100.0	2803	2	Q748V3	Q748v3	geobacter s

ALIGNMENTS

RESULT 1

Q972R5

ID Q972R5 PRELIMINARY; PRT; 130 AA.
 AC Q972R5;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein ST1069.
 GN OrderedLocusNames=ST1069;
 OS Sulfolobus tokodaii.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus.
 OX NCBI_TaxID=111955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JCM 10545 / 7;
 RX MEDLINE=21456156; PubMed=11572479;
 RA Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
 RA Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
 RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
 RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
 RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
 RA Oshima T., Kikuchi H.;
 RT "Complete genome sequence of an aerobic thermoacidophilic
 RT Crenarchaeon, Sulfolobus tokodaii strain7.";
 RL DNA Res. 8:123-140(2001).
 DR EMBL; AP000984; BAB66099.1; -.
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 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 3 HKNQT 7

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 Job time : 179 secs

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Run on: April 28, 2005, 12:06:47 ; Search time 132 Seconds
(without alignments)
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Title: US-09-992-124C-34
Perfect score: 29
Sequence: 1 HKNQT 5

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Gapop 10.0 , Gapext 0.5

Searched: 1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters: 73

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Post-processing: Minimum Match 100%
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Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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9	29	100.0	171	16	US-10-437-963-122535	Sequence 122535,
10	29	100.0	176	17	US-10-722-045-97	Sequence 97, Appl
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12	29	100.0	193	16	US-10-767-701-62389	Sequence 62389, A
13	29	100.0	363	15	US-10-094-749-1983	Sequence 1983, Ap
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ALIGNMENTS

RESULT 1

US-09-867-852-5

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; Sequence 5, Application US/09867852
; Patent No. US20020147324A1
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindrinos, Michael N.
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
; TITLE OF INVENTION: DETECTION METHODS
; FILE REFERENCE: 00786/254002
; CURRENT APPLICATION NUMBER: US/09/867,852
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/301,085
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/310,912
; PRIOR FILING DATE: EARLIER FILING DATE: 1994-09-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/227,360
; PRIOR FILING DATE: EARLIER FILING DATE: 1994-04-13
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-867-852-5

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Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 5 HKNQT 9

Search completed: April 28, 2005, 12:21:01
Job time : 133 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 28, 2005, 12:03:36 ; Search time 41 Seconds
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Title: US-09-992-124C-34
Perfect score: 29
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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; Sequence 5, Application US/08310912A

; Patent No. 5981730

; GENERAL INFORMATION:

; APPLICANT: Ausubel, Frederick M.

; APPLICANT: Staskawicz, Brian J.

; APPLICANT: Brent, Andrew F.

; APPLICANT: Dahlbeck, Douglas

; APPLICANT: Katagiri, Fumiaki

; APPLICANT: Kunkel, Barbara N.

; APPLICANT: Mindrinos, Michael N.

; APPLICANT: Yu, Guo-Liang

; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND DETECTION

; TITLE OF INVENTION: METHODS

; NUMBER OF SEQUENCES: 208
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson P.C.
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02110-2904
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30B
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/310,912A
 ; FILING DATE: September 22, 1994
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/227,360
 ; FILING DATE: April 13, 1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lech, Karen F.
 ; REGISTRATION NUMBER: 35,238
 ; REFERENCE/DOCKET NUMBER: 00786/254001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 542-5070
 ; TELEFAX: (617) 542-8906
 ; TELEX: 100254
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-310-912A-5

Query Match 100.0%; Score 29; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 5;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 5 HKNQT 9

Search completed: April 28, 2005, 12:10:31
 Job time : 41 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 28, 2005, 11:55:21 ; Search time 164 Seconds
(without alignments)
11.791 Million cell updates/sec

Title: US-09-992-124C-34
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Post-processing: Minimum Match 100%
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- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
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- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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23	29	100.0	453	2	AAW42403	Aaw42403	Truncated
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44	29	100.0	505	2	AAy25942	Aay25942	Human ICA
45	29	100.0	505	2	AAy25933	Aay25933	Chimpanze
46	29	100.0	505	2	AAy25943	Aay25943	Human ICA
47	29	100.0	505	2	AAy25939	Aay25939	Human ICA
48	29	100.0	505	2	AAy25945	Aay25945	Chimp ICA
49	29	100.0	505	2	AAy25946	Aay25946	Chimp ICA
50	29	100.0	505	2	AAy25937	Aay25937	Human ICA
51	29	100.0	505	2	AAy25941	Aay25941	Human ICA
52	29	100.0	505	2	AAy25940	Aay25940	Human ICA
53	29	100.0	505	3	AAB15091	Aab15091	Human int
54	29	100.0	505	3	AAW90880	Aaw90880	Chimpanze
55	29	100.0	505	5	AAM50634	Aam50634	Gorilla i
56	29	100.0	505	5	AAM50635	Aam50635	Orangutan
57	29	100.0	505	5	AAM50628	Aam50628	Chimpanze
58	29	100.0	505	5	AAM50631	Aam50631	Human int
59	29	100.0	505	6	ABU07294	Abu07294	Human exp
60	29	100.0	505	6	ABU07297	Abu07297	Human exp
61	29	100.0	505	6	ABU07271	Abu07271	Human exp
62	29	100.0	505	6	ABU07296	Abu07296	Human exp
63	29	100.0	505	6	ABU07300	Abu07300	Human exp
64	29	100.0	505	6	ABU07299	Abu07299	Human exp
65	29	100.0	505	6	ABU07295	Abu07295	Human exp
66	29	100.0	505	6	ABU07298	Abu07298	Human exp

67	29	100.0	505	7	ADE97403	Ade97403	Chimpanze
68	29	100.0	507	2	AAR48038	Aar48038	ICAM-1. 3
69	29	100.0	507	2	AAW42331	Aaw42331	Mutant of
70	29	100.0	507	2	AAW42332	Aaw42332	G380C mut
71	29	100.0	507	2	AAW42325	Aaw42325	T304C mut
72	29	100.0	507	2	AAW42333	Aaw42333	W382C mut
73	29	100.0	507	2	AAW42327	Aaw42327	Mutant of
74	29	100.0	507	2	AAW42329	Aaw42329	E375C mut
75	29	100.0	507	2	AAW42326	Aaw42326	K306C mut
76	29	100.0	507	2	AAW42330	Aaw42330	D377C mut
77	29	100.0	507	2	AAW42328	Aaw42328	A309C mut
78	29	100.0	507	2	AAW42334	Aaw42334	T429C mut
79	29	100.0	507	2	AAW71286	Aaw71286	Human int
80	29	100.0	507	2	AAW71285	Aaw71285	Human int
81	29	100.0	507	2	AAW94407	Aaw94407	Transmemb
82	29	100.0	507	6	ABU07278	Abu07278	Human exp
83	29	100.0	507	6	ABU07291	Abu07291	Human exp
84	29	100.0	507	6	ABU07276	Abu07276	Human exp
85	29	100.0	507	6	ABU07281	Abu07281	Human exp
86	29	100.0	507	6	ABU07275	Abu07275	Human exp
87	29	100.0	507	6	ABU07279	Abu07279	Human exp
88	29	100.0	507	6	ABU07284	Abu07284	Human exp
89	29	100.0	507	6	ABU07292	Abu07292	Human exp
90	29	100.0	507	6	ABU07293	Abu07293	Human exp
91	29	100.0	507	6	ABU07283	Abu07283	Human exp
92	29	100.0	507	6	ABU07277	Abu07277	Human exp
93	29	100.0	507	6	ABU07280	Abu07280	Human exp
94	29	100.0	507	6	ABU07274	Abu07274	Human exp
95	29	100.0	507	6	ABU07282	Abu07282	Human exp
96	29	100.0	508	2	AAW14721	Aaw14721	Human ICA
97	29	100.0	508	6	ABU04076	Abu04076	Human exp
98	29	100.0	509	2	AAW71269	Aaw71269	Human int
99	29	100.0	509	6	ABU07290	Abu07290	Human exp
100	29	100.0	531	2	AAR80110	Aar80110	ICAM-1 CD
101	29	100.0	531	4	ABG00802	Abg00802	Novel hum
102	29	100.0	531	6	ABU04070	Abu04070	Human exp
103	29	100.0	532	1	AAP91357	Aap91357	Intercell
104	29	100.0	532	2	AAR04165	Aar04165	Inter-cel
105	29	100.0	532	2	AAR20809	Aar20809	Intercell
106	29	100.0	532	2	AAR58779	Aar58779	Inter-cel
107	29	100.0	532	2	AAR46066	Aar46066	Human ICA
108	29	100.0	532	2	AAR79457	Aar79457	ICAM-1. 1
109	29	100.0	532	2	AAR90294	Aar90294	Intracell
110	29	100.0	532	2	AAR91437	Aar91437	Human ICA
111	29	100.0	532	2	AAW14720	Aaw14720	Human ICA
112	29	100.0	532	2	AAW09313	Aaw09313	Human ICA
113	29	100.0	532	2	AAW27270	Aaw27270	Human int
114	29	100.0	532	2	AAW71263	Aaw71263	Human int
115	29	100.0	532	2	AAW70871	Aaw70871	Intracell
116	29	100.0	532	2	AAW80446	Aaw80446	Human int
117	29	100.0	532	2	AAW46735	Aaw46735	Amino aci
118	29	100.0	532	2	AAW86193	Aaw86193	Human int
119	29	100.0	532	3	AAV96132	Aay96132	Human int
120	29	100.0	532	3	AAV59499	Aay59499	Human ICA
121	29	100.0	532	4	AAU02441	Aau02441	Human int
122	29	100.0	532	5	AAM47849	Aam47849	Human ICA
123	29	100.0	532	5	ABB76147	Abb76147	Human int

124	29	100.0	532	5	ABP53763	Abp53763	Human	int
125	29	100.0	532	6	ABU04079	Abu04079	Human	exp
126	29	100.0	532	6	ABU04086	Abu04086	Human	exp
127	29	100.0	532	6	ABU04088	Abu04088	Human	exp
128	29	100.0	532	6	ABU04077	Abu04077	Human	exp
129	29	100.0	532	6	ABU04085	Abu04085	Human	exp
130	29	100.0	532	6	ABU04056	Abu04056	Human	exp
131	29	100.0	532	6	ABU04059	Abu04059	Human	exp
132	29	100.0	532	6	ABU04067	Abu04067	Human	exp
133	29	100.0	532	6	ABU04073	Abu04073	Human	exp
134	29	100.0	532	6	ABU04057	Abu04057	Human	exp
135	29	100.0	532	6	ABU04063	Abu04063	Human	exp
136	29	100.0	532	6	ABU04068	Abu04068	Human	exp
137	29	100.0	532	6	ABU04055	Abu04055	Human	exp
138	29	100.0	532	6	ABU04069	Abu04069	Human	exp
139	29	100.0	532	6	ABU04071	Abu04071	Human	exp
140	29	100.0	532	6	ABU04075	Abu04075	Human	exp
141	29	100.0	532	6	ABU04065	Abu04065	Human	exp
142	29	100.0	532	6	ABU04082	Abu04082	Human	exp
143	29	100.0	532	6	ABU04060	Abu04060	Human	exp
144	29	100.0	532	6	ABU04078	Abu04078	Human	exp
145	29	100.0	532	6	ABU04072	Abu04072	Human	exp
146	29	100.0	532	6	ABU04074	Abu04074	Human	exp
147	29	100.0	532	6	ABU04080	Abu04080	Human	exp
148	29	100.0	532	6	ABU04081	Abu04081	Human	exp
149	29	100.0	532	6	ABU04084	Abu04084	Human	exp
150	29	100.0	532	7	ADC38970	Adc38970	Human	ICA
151	29	100.0	532	7	ADD25580	Add25580	Binding d	
152	29	100.0	532	7	ADE55755	Ade55755	Human	Pro
153	29	100.0	532	7	ADE55751	Ade55751	Human	Pro
154	29	100.0	532	7	ADE97333	Ade97333	Human	int
155	29	100.0	532	7	ADE97385	Ade97385	Human	int
156	29	100.0	532	7	ADN95576	Adn95576	Human	BEC
157	29	100.0	532	8	ADJ78598	Adj78598	Human	ICA
158	29	100.0	532	8	ADJ75299	Adj75299	Marker ge	
159	29	100.0	532	8	ADM46542	Adm46542	Human	int
160	29	100.0	532	8	ADL82815	Adl82815	Human	PRO
161	29	100.0	532	8	ADO49352	Ado49352	Human	ICA
162	29	100.0	532	8	ADO19299	Ado19299	Human	PRO
163	29	100.0	532	8	ADO19301	Ado19301	Human	PRO
164	29	100.0	532	8	ADP45603	Adp45603	Human	int
165	29	100.0	532	8	ADQ76214	Adq76214	Chemokine	
166	29	100.0	532	8	ADR31183	Adr31183	Human	ICA
167	29	100.0	532	8	ADR31198	Adr31198	Human	ICA
168	29	100.0	532	8	ADR31162	Adr31162	Human	ICA
169	29	100.0	532	8	ADR31208	Adr31208	Human	ICA
170	29	100.0	532	8	ADR31210	Adr31210	Human	ICA
171	29	100.0	532	8	ADR31166	Adr31166	Human	ICA
172	29	100.0	532	8	ADR31173	Adr31173	Human	ICA
173	29	100.0	532	8	ADR31175	Adr31175	Human	ICA
174	29	100.0	532	8	ADR31189	Adr31189	Human	ICA
175	29	100.0	532	8	ADR31200	Adr31200	Human	ICA
176	29	100.0	532	8	ADR31213	Adr31213	Human	ICA
177	29	100.0	532	8	ADR31149	Adr31149	Human	ICA
178	29	100.0	532	8	ADR31152	Adr31152	Human	ICA
179	29	100.0	532	8	ADR31177	Adr31177	Human	ICA
180	29	100.0	532	8	ADR31181	Adr31181	Human	ICA

181	29	100.0	532	8	ADR31187	Adr31187	Human	ICA
182	29	100.0	532	8	ADR31203	Adr31203	Human	ICA
183	29	100.0	532	8	ADR31140	Adr31140	Human	ICA
184	29	100.0	532	8	ADR31154	Adr31154	Human	ICA
185	29	100.0	532	8	ADR31157	Adr31157	Human	ICA
186	29	100.0	532	8	ADR31165	Adr31165	Human	ICA
187	29	100.0	532	8	ADR31168	Adr31168	Human	ICA
188	29	100.0	532	8	ADR31214	Adr31214	Human	ICA
189	29	100.0	532	8	ADR31158	Adr31158	Human	ICA
190	29	100.0	532	8	ADR31171	Adr31171	Human	ICA
191	29	100.0	532	8	ADR31172	Adr31172	Human	ICA
192	29	100.0	532	8	ADR31191	Adr31191	Human	ICA
193	29	100.0	532	8	ADR31192	Adr31192	Human	ICA
194	29	100.0	532	8	ADR31167	Adr31167	Human	ICA
195	29	100.0	532	8	ADR31199	Adr31199	Human	ICA
196	29	100.0	532	8	ADR31201	Adr31201	Human	ICA
197	29	100.0	532	8	ADR31156	Adr31156	Human	ICA
198	29	100.0	532	8	ADR31195	Adr31195	Human	ICA
199	29	100.0	532	8	ADR31197	Adr31197	Human	ICA
200	29	100.0	532	8	ADR31211	Adr31211	Human	ICA
201	29	100.0	532	8	ADR31147	Adr31147	Human	ICA
202	29	100.0	532	8	ADR31159	Adr31159	Human	ICA
203	29	100.0	532	8	ADR31161	Adr31161	Human	ICA
204	29	100.0	532	8	ADR31170	Adr31170	Human	ICA
205	29	100.0	532	8	ADR31182	Adr31182	Human	ICA
206	29	100.0	532	8	ADR31206	Adr31206	Human	ICA
207	29	100.0	532	8	ADR31139	Adr31139	Human	ICA
208	29	100.0	532	8	ADR31141	Adr31141	Human	ICA
209	29	100.0	532	8	ADR31178	Adr31178	Human	ICA
210	29	100.0	532	8	ADR31179	Adr31179	Human	ICA
211	29	100.0	532	8	ADR31215	Adr31215	Human	ICA
212	29	100.0	532	8	ADR31143	Adr31143	Human	ICA
213	29	100.0	532	8	ADR31160	Adr31160	Human	ICA
214	29	100.0	532	8	ADR31163	Adr31163	Human	ICA
215	29	100.0	532	8	ADR31180	Adr31180	Human	ICA
216	29	100.0	532	8	ADR31202	Adr31202	Human	ICA
217	29	100.0	532	8	ADR31207	Adr31207	Human	ICA
218	29	100.0	532	8	ADR31212	Adr31212	Human	ICA
219	29	100.0	532	8	ADR31142	Adr31142	Human	ICA
220	29	100.0	532	8	ADR31153	Adr31153	Human	ICA
221	29	100.0	532	8	ADR31185	Adr31185	Human	ICA
222	29	100.0	532	8	ADR31132	Adr31132	Human	ICA
223	29	100.0	532	8	ADR31155	Adr31155	Human	ICA
224	29	100.0	532	8	ADR31188	Adr31188	Human	ICA
225	29	100.0	532	8	ADR31190	Adr31190	Human	ICA
226	29	100.0	532	8	ADR31205	Adr31205	Human	ICA
227	29	100.0	532	8	ADR31144	Adr31144	Human	ICA
228	29	100.0	532	8	ADR31148	Adr31148	Human	ICA
229	29	100.0	532	8	ADR31184	Adr31184	Human	ICA
230	29	100.0	532	8	ADR31194	Adr31194	Human	ICA
231	29	100.0	532	8	ADR31209	Adr31209	Human	ICA
232	29	100.0	532	8	ADR31145	Adr31145	Human	ICA
233	29	100.0	532	8	ADR31146	Adr31146	Human	ICA
234	29	100.0	532	8	ADR31150	Adr31150	Human	ICA
235	29	100.0	532	8	ADR31169	Adr31169	Human	ICA
236	29	100.0	532	8	ADR31174	Adr31174	Human	ICA
237	29	100.0	532	8	ADR31176	Adr31176	Human	ICA

238	29	100.0	532	8	ADR31186	Adr31186	Human	ICA
239	29	100.0	532	8	ADR31193	Adr31193	Human	ICA
240	29	100.0	532	8	ADR31196	Adr31196	Human	ICA
241	29	100.0	532	8	ADR31204	Adr31204	Human	ICA
242	29	100.0	532	8	ADR31216	Adr31216	Human	ICA
243	29	100.0	532	8	ADQ39788	Adq39788	Human	myo
244	29	100.0	532	8	ADR97011	Adr97011	Human	ICA
245	29	100.0	532	8	ADR97015	Adr97015	Human	ICA
246	29	100.0	532	8	ADR97039	Adr97039	Human	ICA
247	29	100.0	532	8	ADR96990	Adr96990	Human	ICA
248	29	100.0	532	8	ADR96993	Adr96993	Human	ICA
249	29	100.0	532	8	ADR97016	Adr97016	Human	ICA
250	29	100.0	532	8	ADR97026	Adr97026	Human	ICA
251	29	100.0	532	8	ADR97036	Adr97036	Human	ICA
252	29	100.0	532	8	ADR97045	Adr97045	Human	ICA
253	29	100.0	532	8	ADR96976	Adr96976	Human	ICA
254	29	100.0	532	8	ADR96980	Adr96980	Human	ICA
255	29	100.0	532	8	ADR96982	Adr96982	Human	ICA
256	29	100.0	532	8	ADR96991	Adr96991	Human	ICA
257	29	100.0	532	8	ADR96995	Adr96995	Human	ICA
258	29	100.0	532	8	ADR97002	Adr97002	Human	ICA
259	29	100.0	532	8	ADR97003	Adr97003	Human	ICA
260	29	100.0	532	8	ADR97048	Adr97048	Human	ICA
261	29	100.0	532	8	ADR96977	Adr96977	Human	ICA
262	29	100.0	532	8	ADR96983	Adr96983	Human	ICA
263	29	100.0	532	8	ADR96999	Adr96999	Human	ICA
264	29	100.0	532	8	ADR97019	Adr97019	Human	ICA
265	29	100.0	532	8	ADR97021	Adr97021	Human	ICA
266	29	100.0	532	8	ADR97024	Adr97024	Human	ICA
267	29	100.0	532	8	ADR97043	Adr97043	Human	ICA
268	29	100.0	532	8	ADR97031	Adr97031	Human	ICA
269	29	100.0	532	8	ADR97042	Adr97042	Human	ICA
270	29	100.0	532	8	ADR97000	Adr97000	Human	ICA
271	29	100.0	532	8	ADR97005	Adr97005	Human	ICA
272	29	100.0	532	8	ADR97028	Adr97028	Human	ICA
273	29	100.0	532	8	ADR97044	Adr97044	Human	ICA
274	29	100.0	532	8	ADR96998	Adr96998	Human	ICA
275	29	100.0	532	8	ADR97027	Adr97027	Human	ICA
276	29	100.0	532	8	ADR97047	Adr97047	Human	ICA
277	29	100.0	532	8	ADR96979	Adr96979	Human	ICA
278	29	100.0	532	8	ADR96989	Adr96989	Human	ICA
279	29	100.0	532	8	ADR96994	Adr96994	Human	ICA
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281	29	100.0	532	8	ADR97008	Adr97008	Human	ICA
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283	29	100.0	532	8	ADR97013	Adr97013	Human	ICA
284	29	100.0	532	8	ADR97030	Adr97030	Human	ICA
285	29	100.0	532	8	ADR97038	Adr97038	Human	ICA
286	29	100.0	532	8	ADR97041	Adr97041	Human	ICA
287	29	100.0	532	8	ADR97051	Adr97051	Human	ICA
288	29	100.0	532	8	ADR97053	Adr97053	Human	ICA
289	29	100.0	532	8	ADR96969	Adr96969	Human	ICA
290	29	100.0	532	8	ADR97018	Adr97018	Human	ICA
291	29	100.0	532	8	ADR97025	Adr97025	Human	ICA
292	29	100.0	532	8	ADR97040	Adr97040	Human	ICA
293	29	100.0	532	8	ADR97052	Adr97052	Human	ICA
294	29	100.0	532	8	ADR96986	Adr96986	Human	ICA

295	29	100.0	532	8	ADR97022	Adr97022	Human	ICA
296	29	100.0	532	8	ADR97032	Adr97032	Human	ICA
297	29	100.0	532	8	ADR97033	Adr97033	Human	ICA
298	29	100.0	532	8	ADR96978	Adr96978	Human	ICA
299	29	100.0	532	8	ADR96985	Adr96985	Human	ICA
300	29	100.0	532	8	ADR96987	Adr96987	Human	ICA
301	29	100.0	532	8	ADR96992	Adr96992	Human	ICA
302	29	100.0	532	8	ADR97012	Adr97012	Human	ICA
303	29	100.0	532	8	ADR96981	Adr96981	Human	ICA
304	29	100.0	532	8	ADR96997	Adr96997	Human	ICA
305	29	100.0	532	8	ADR97004	Adr97004	Human	ICA
306	29	100.0	532	8	ADR97020	Adr97020	Human	ICA
307	29	100.0	532	8	ADR97029	Adr97029	Human	ICA
308	29	100.0	532	8	ADR97035	Adr97035	Human	ICA
309	29	100.0	532	8	ADR96984	Adr96984	Human	ICA
310	29	100.0	532	8	ADR97010	Adr97010	Human	ICA
311	29	100.0	532	8	ADR97023	Adr97023	Human	ICA
312	29	100.0	532	8	ADR97037	Adr97037	Human	ICA
313	29	100.0	532	8	ADR97049	Adr97049	Human	ICA
314	29	100.0	532	8	ADR97050	Adr97050	Human	ICA
315	29	100.0	532	8	ADR97006	Adr97006	Human	ICA
316	29	100.0	532	8	ADR97014	Adr97014	Human	ICA
317	29	100.0	532	8	ADR97007	Adr97007	Human	ICA
318	29	100.0	532	8	ADR97017	Adr97017	Human	ICA
319	29	100.0	532	8	ADR97034	Adr97034	Human	ICA
320	29	100.0	532	8	ADR97046	Adr97046	Human	ICA
321	29	100.0	532	8	ADS34916	Ads34916	Human	aut
322	29	100.0	533	8	ADR31151	Adr31151	Human	ICA
323	29	100.0	533	8	ADR31164	Adr31164	Human	ICA
324	29	100.0	533	8	ADR97001	Adr97001	Human	ICA
325	29	100.0	533	8	ADR96988	Adr96988	Human	ICA
326	29	100.0	562	1	AAP80458	Aap80458	Sequence	
327	29	100.0	562	6	ABU04062	Abu04062	Human	exp
328	29	100.0	613	4	AAB95548	Aab95548	Human	pro
329	29	100.0	613	4	AAM94035	Aam94035	Human	sto
330	29	100.0	677	8	ADS44729	Ads44729	Bacterial	
331	29	100.0	680	2	AAR48037	Aar48037	tICAM(453	
332	29	100.0	680	6	ABU07273	Abu07273	Human	exp
333	29	100.0	799	5	AAM47852	Aam47852	Human	ICA
334	29	100.0	799	7	ADE97339	Ade97339	Human	chi
335	29	100.0	822	5	AAM47865	Aam47865	Human	ICA
336	29	100.0	822	7	ADE97371	Ade97371	Immunoadh	
337	29	100.0	965	2	AAR83440	Aar83440	A.thalian	
338	29	100.0	1020	8	ADN22798	Adn22798	Bacterial	
339	29	100.0	1075	2	AAR38861	Aar38861	GC-C. 2/1	
340	29	100.0	1158	8	ADR88899	Adr88899	Anopheles	
341	29	100.0	1537	8	ADS44355	Ads44355	Bacterial	
342	29	100.0	2201	3	AAAY79380	Aay79380	Human	ATP
343	29	100.0	2201	4	AAM50227	Aam50227	Human	ATP
344	29	100.0	2201	4	AAE13021	Aae13021	Human	ATP
345	29	100.0	2201	4	ADG20598	Adg20598	Human	ABC
346	29	100.0	2201	5	ABP65164	Abp65164	Hypoxia-r	
347	29	100.0	2201	7	ADD89025	Add89025	TAT265. 1	
348	29	100.0	2201	8	ADJ45473	Adj45473	LXR-ligan	
349	29	100.0	2201	8	ADQ39361	Adq39361	Human	myo
350	29	100.0	2201	8	ADQ39364	Adq39364	Human	myo
351	29	100.0	2233	4	ADG20599	Adg20599	Human	ABC

352	29	100.0	2256	6	ABR40000	Abr40000	Human	ABC
353	29	100.0	2259	3	AAB38107	Aab38107	Human	ABC
354	29	100.0	2260	3	AAB38106	Aab38106	Human	ABC
355	29	100.0	2261	3	AAB38111	Aab38111	Human	ABC
356	29	100.0	2261	3	AAB38110	Aab38110	Human	ABC
357	29	100.0	2261	3	AAB38117	Aab38117	Human	ABC
358	29	100.0	2261	3	AAB38115	Aab38115	Human	ABC
359	29	100.0	2261	3	AAB38113	Aab38113	Human	ABC
360	29	100.0	2261	3	AAB38116	Aab38116	Human	ABC
361	29	100.0	2261	3	AAB38114	Aab38114	Human	ABC
362	29	100.0	2261	3	AAB38109	Aab38109	Human	ABC
363	29	100.0	2261	3	AAB38082	Aab38082	Human	ABC
364	29	100.0	2261	3	AAB38105	Aab38105	Human	ABC
365	29	100.0	2261	3	AAB38112	Aab38112	Human	ABC
366	29	100.0	2261	3	AAB38104	Aab38104	Human	ABC
367	29	100.0	2261	4	AAB71749	Aab71749	Human	ABC
368	29	100.0	2261	4	AAM50228	Aam50228	Human	ATP
369	29	100.0	2261	4	AAE13022	Aae13022	Human	ATP
370	29	100.0	2261	4	AAM78550	Aam78550	Human	pro
371	29	100.0	2261	4	AAB31362	Aab31362	Amino	aci
372	29	100.0	2261	4	AAB31361	Aab31361	Amino	aci
373	29	100.0	2261	4	AAB31363	Aab31363	Amino	aci
374	29	100.0	2261	4	AAB31366	Aab31366	Amino	aci
375	29	100.0	2261	4	AAB31365	Aab31365	Amino	aci
376	29	100.0	2261	4	AAB31367	Aab31367	Amino	aci
377	29	100.0	2261	4	AAU02176	Aau02176	Human	ABC
378	29	100.0	2261	4	AAU02183	Aau02183	Human	ABC
379	29	100.0	2261	4	AAU02188	Aau02188	Human	ABC
380	29	100.0	2261	4	AAU02189	Aau02189	Human	ABC
381	29	100.0	2261	4	AAU02182	Aau02182	Human	ABC
382	29	100.0	2261	4	AAU02186	Aau02186	Human	ABC
383	29	100.0	2261	4	AAU02181	Aau02181	Human	ABC
384	29	100.0	2261	4	AAU02177	Aau02177	Human	ABC
385	29	100.0	2261	5	AAE23000	Aae23000	Human	ABC
386	29	100.0	2261	5	ABP52092	Abp52092	Homo sapi	
387	29	100.0	2261	5	ABB83120	Abb83120	Polymorph	
388	29	100.0	2261	5	ABB83118	Abb83118	Polymorph	
389	29	100.0	2261	5	ABB83116	Abb83116	Polymorph	
390	29	100.0	2261	5	ABB83124	Abb83124	Polymorph	
391	29	100.0	2261	5	ABB83121	Abb83121	Polymorph	
392	29	100.0	2261	5	ABB83122	Abb83122	Polymorph	
393	29	100.0	2261	5	ABB83111	Abb83111	Human	ABC
394	29	100.0	2261	5	ABB83119	Abb83119	Polymorph	
395	29	100.0	2261	5	ABB83123	Abb83123	Polymorph	
396	29	100.0	2261	5	ABB83117	Abb83117	Polymorph	
397	29	100.0	2261	5	ABB83115	Abb83115	Polymorph	
398	29	100.0	2261	5	ABB81578	Abb81578	Human	ABC
399	29	100.0	2261	6	ABU11899	Abu11899	Human	ATP
400	29	100.0	2261	6	ABR62034	Abr62034	Human	ABC
401	29	100.0	2261	6	ABR62033	Abr62033	Human	ABC
402	29	100.0	2261	7	ADE85895	Ade85895	Human	ATP
403	29	100.0	2261	7	ADP65173	Adp65173	Human	ATP
404	29	100.0	2261	8	ADP23550	Adp23550	PRO	polyp
405	29	100.0	2261	8	ADQ39363	Adq39363	Human	myo
406	29	100.0	2263	4	ABB11956	Abb11956	Human	ABC
407	29	100.0	2263	4	AAM79534	Aam79534	Human	pro

ALIGNMENTS

RESULT 1

ABP51729

ID ABP51729 standard; peptide; 5 AA.

XX

AC ABP51729;

XX

DT 01-OCT-2002 (first entry)

XX

DE ICAM 1 cell surface protein peptide.

XX

KW Human; epidermal growth factor receptor; EGFR; immunogenic; cancer;
KW apoptosis; cytostatic; cell surface protein.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO200247613-A2.

XX

PD 20-JUN-2002.

XX

PF 13-NOV-2001; 2001WO-US047734.

XX

PR 27-NOV-2000; 2000US-00723307.

XX

PA (NOUN) UNIV NORTHWESTERN.

XX

PI Calenoff E, Ditlow CC;

XX

DR WPI; 2002-566624/60.

XX

PT Candidates for cancer-specific or cancer-associated antigens useful for
PT diagnosis and treatment of cancer comprise synthetic peptides.

XX

PS Disclosure; Page 16; 53pp; English.

XX

CC The present invention describes a method for identifying candidates that
CC are cancer-specific or cancer-associated antigens. The method involves:
CC (1) mapping hydrophilic regions of amino acid sequences; (2) identifying
CC hydrophilic peptide regions that are glycosylated in non-cancerous cells,
CC but deglycosylated in cancer cells; and (3) synthesising, labeling and
CC testing peptides. The cancer-specific/associated antigen sequences have
CC cytostatic activity, and can be used for promoting cancer cell apoptosis.
CC The method can be used for identifying candidates that are cancer-
CC specific or cancer-associated antigens for use in the diagnosis and
CC treatment of cancer. The method involves the use of a site of
CC deglycosylated amino acids in the cancer cells, and so confers a cancer-
CC specific or highly cancer-associated immunogenicity or marker function to
CC the peptide and avoiding self-recognition. The peptides are further not
CC intracellularly expressed, but are located on the cell surfaces
CC (predictably secreted or released into pericellular fluids) in sufficient
CC numbers, and so are sufficiently accessible for targeting T cells; and
CC are present at the earlier stages of cancer progression as well as during
CC later stages; and are retained on the surface of the cancer cells for a

CC time sufficient for the therapeutic T cells to find their target and
CC retain the bound T cells for a time sufficient to affect cancer cell
CC death. ABP51697 to ABP51771 represent amino acid sequence used in the
CC exemplification of the present invention

XX

SQ Sequence 5 AA;

Query Match 100.0%; Score 29; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKNQT 5

|||||

Db 1 HKNQT 5

RESULT 2

AAO30011

ID AAO30011 standard; peptide; 5 AA.

XX

AC AAO30011;

XX

DT 03-SEP-2003 (first entry)

XX

DE Peptide #19 used to enhance cell secretion.

XX

KW Cellular adhesion; growth; expression; secretion.

XX

OS Unidentified.

XX

PN WO2003044045-A2.

XX

PD 30-MAY-2003.

XX

PF 19-NOV-2002; 2002WO-US037207.

XX

PR 19-NOV-2001; 2001US-00992124.

XX

PA (BECT) BECTON DICKINSON & CO.

XX

PI Campbell RL, Heidaran M, Spargo CA, Wilkins JH, Haaland PD;

XX

DR WPI; 2003-482396/45.

XX

PT New peptide, useful for enhancing cell growth and/or secretion in a cell
PT culture system.

XX

PS Claim 4; Page 45; 78pp; English.

XX

CC The invention relates to peptides having cell adhesion, growth,
CC expression or secretion-enhancing activities. The peptides of the
CC invention are useful for enhancing cell growth and/or secretion in a cell
CC culture system. The present sequence is a peptide used to enhance cell
CC secretion. Note: This sequence SEQ ID NO:34 is stated to be similar to
CC the sequence shown in page 66 (AAO30049). However these sequences differ

XX

SQ Sequence 5 AA;

Query Match 100.0%; Score 29; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKNQT 5
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Db 1 HKNQT 5

RESULT 3

AAR80135

ID AAR80135 standard; protein; 11 AA.

XX

AC AAR80135;

XX

DT 20-APR-1996 (first entry)

XX

DE Rps2 disease resistance polypeptide.

XX

KW RPS2; transgenic plant; Pseudomonas syringae plant pathogen;

KW disease resistance; crop improvement; Arabidopsis; tomato; soybean; bean;

KW maize; wheat; rice.

XX

OS Arabidopsis thaliana.

XX

PN WO9528478-A1.

XX

PD 26-OCT-1995.

XX

PF 13-APR-1995; 95WO-US004570.

XX

PR 13-APR-1994; 94US-00227360.

XX

PA (GEHO) GEN HOSPITAL CORP.

PA (REGC) UNIV CALIFORNIA.

XX

PI Ausubel FM, Staskawicz BJ, Bent AF, Dahlbeck D, Katagiri F;

PI Kunkel BN, Mindrinos MN, Yu G;

XX

DR WPI; 1995-373794/48.

DR N-PSDB; AAT04798.

XX

PT Pure DNA encoding an Arabidopsis thaliana Rps2 polypeptide - used to
PT express the polypeptide in plant cells to provide disease resistance to
PT pathogens.

XX

PS Claim 6; Page 45; 88pp; English.

XX

CC DNA encoding the Rps2 disease resistance polypeptide (see also AAR80132-
CC 34) can be used to transform a plant cell which is subsequently
CC propagated into a transgenic plant exhibiting resistance to diseases
CC caused by plant pathogens carrying an avirulence gene generating signal
CC recognized by an Rps polypeptide. Specifically, the plant pathogen is
CC Pseudomonas syringae which carries the avrRpt2 avirulence gene (See
CC AAT04799). The plant is a crop plant, especially tomato, soybean, bean,
CC maize, wheat, rice and Arabidopsis

XX

SQ Sequence 11 AA;

Query Match 100.0%; Score 29; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 10;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKNQT 5

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Db 5 HKNQT 9

Search completed: April 28, 2005, 12:09:50

Job time : 171 secs